

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/546,000  
Source: PCT  
Date Processed by STIC: 08/29/2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 08/29/2005

PATENT APPLICATION: US/10/546,000

TIME: 18:10:22

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\08292005\J546000.raw

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4 <110> APPLICANT: Hamada, Hirofumi
5     Ito, Yoshinori
6     Takahashi, Kazuhiro
7     Morikawa, Masayuki
9 <120> TITLE OF INVENTION: Methods For Treating Ischemic Diseases
12 <130> FILE REFERENCE: 50026/054001
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/546,000
C--> 14 <141> CURRENT FILING DATE: 2005-08-18
14 <150> PRIOR APPLICATION NUMBER: PCT/JP04/000957
15 <151> PRIOR FILING DATE: 2004-01-30
17 <150> PRIOR APPLICATION NUMBER: JP 2003-040806
18 <151> PRIOR FILING DATE: 2003-02-19
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3372
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(3372)
33 <400> SEQUENCE: 1
34 atg gac tct tta gcc agc tta gtt ctc tgt gga gtc agc ttg ctc ctt      48
35 Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu
36 1          5          10          15
38 tct gga act gtg gaa ggt gcc atg gac ttg atc ttg atc aat tcc cta      96
39 Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
40          20          25          30
42 cct ctt gta tct gat gct gaa aca tct ctc acc tgc att gcc tct ggg      144
43 Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
44          35          40          45
46 tgg cgc ccc cat gag ccc atc acc ata gga agg gac ttt gaa gcc tta      192
47 Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
48          50          55          60
50 atg aac cag cac cag gat ccg ctg gaa gtt act caa gat gtg acc aga      240
51 Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
52 65          70          75          80
54 gaa tgg gct aaa aaa gtt gtt tgg aag aga gaa aag gct agt aag atc      288
55 Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
56          85          90          95
58 aat ggt gct tat ttc tgt gaa ggg cga gtt cga gga gag gca atc agg      336
59 Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
60          100          105          110

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62 ata cga acc atg aag atg cgt caa caa gct tcc ttc cta cca gct act 384
63 Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
64      115      120      125
66 tta act atg act gtg gac aag gga gat aac gtg aac ata tct ttc aaa 432
67 Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
68      130      135      140
70 aag gta ttg att aaa gaa gaa gat gca gtg att tac aaa aat ggt tcc 480
71 Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
72 145      150      155      160
74 ttc atc cat tca gtg ccc cgg cat gaa gta cct gat att cta gaa gta 528
75 Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
76      165      170      175
78 cac ctg cct cat gct cag ccc cag gat gct gga gtg tac tcg gcc agg 576
79 His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
80      180      185      190
82 tat ata gga gga aac ctc ttc acc tcg gcc ttc acc agg ctg ata gtc 624
83 Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
84      195      200      205
86 cgg aga tgt gaa gcc cag aag tgg gga cct gaa tgc aac cat ctc tgt 672
87 Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
88      210      215      220
90 act gct tgt atg aac aat ggt gtc tgc cat gaa gat act gga gaa tgc 720
91 Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys
92 225      230      235      240
94 att tgc cct cct ggg ttt atg gga agg acg tgt gag aag gct tgt gaa 768
95 Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu
96      245      250      255
98 ctg cac acg ttt ggc aga act tgt aaa gaa agg tgc agt gga caa gag 816
99 Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu
100      260      265      270
102 gga tgc aag tct tat gtg ttc tgt ctc cct gac ccc tat ggg tgt tcc 864
103 Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser
104      275      280      285
106 tgt gcc aca ggc tgg aag ggt ctg cag tgc aat gaa gca tgc cac cct 912
107 Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro
108      290      295      300
110 ggt ttt tac ggg cca gat tgt aag ctt agg tgc agc tgc aac aat ggg 960
111 Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly
112 305      310      315      320
114 gag atg tgt gat cgc ttc caa gga tgt ctc tgc tct cca gga tgg cag 1008
115 Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln
116      325      330      335
118 ggg ctc cag tgt gag aga gaa ggc ata ccg agg atg acc cca aag ata 1056
119 Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile
120      340      345      350
122 gtg gat ttg cca gat cat ata gaa gta aac agt ggt aaa ttt aat ccc 1104
123 Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro
124      355      360      365
126 att tgc aaa gct tct ggc tgg ccg cta cct act aat gaa gaa atg acc 1152

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127	Ile	Cys	Lys	Ala	Ser	Gly	Trp	Pro	Leu	Pro	Thr	Asn	Glu	Glu	Met	Thr	
128		370					375					380					
130	ctg	gtg	aag	ccg	gat	ggg	aca	gtg	ctc	cat	cca	aaa	gac	ttt	aac	cat	1200
131	Leu	Val	Lys	Pro	Asp	Gly	Thr	Val	Leu	His	Pro	Lys	Asp	Phe	Asn	His	
132	385					390					395				400		
134	acg	gat	cat	ttc	tca	gta	gcc	ata	ttc	acc	atc	cac	cgg	atc	ctc	ccc	1248
135	Thr	Asp	His	Phe	Ser	Val	Ala	Ile	Phe	Thr	Ile	His	Arg	Ile	Leu	Pro	
136					405					410					415		
138	cct	gac	tca	gga	gtt	tgg	gtc	tgc	agt	gtg	aac	aca	gtg	gct	ggg	atg	1296
139	Pro	Asp	Ser	Gly	Val	Trp	Val	Cys	Ser	Val	Asn	Thr	Val	Ala	Gly	Met	
140				420						425				430			
142	gtg	gaa	aag	ccc	ttc	aac	att	tct	gtt	aaa	gtt	ctt	cca	aag	ccc	ctg	1344
143	Val	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Val	Lys	Val	Leu	Pro	Lys	Pro	Leu	
144			435						440				445				
146	aat	gcc	cca	aac	gtg	att	gac	act	gga	cat	aac	ttt	gct	gtc	atc	aac	1392
147	Asn	Ala	Pro	Asn	Val	Ile	Asp	Thr	Gly	His	Asn	Phe	Ala	Val	Ile	Asn	
148		450					455				460						
150	atc	agc	tct	gag	cct	tac	ttt	ggg	gat	gga	cca	atc	aaa	tcc	aag	aag	1440
151	Ile	Ser	Ser	Glu	Pro	Tyr	Phe	Gly	Asp	Gly	Pro	Ile	Lys	Ser	Lys	Lys	
152	465					470					475					480	
154	ctt	cta	tac	aaa	ccc	gtt	aat	cac	tat	gag	gct	tgg	caa	cat	att	caa	1488
155	Leu	Leu	Tyr	Lys	Pro	Val	Asn	His	Tyr	Glu	Ala	Trp	Gln	His	Ile	Gln	
156				485						490					495		
158	gtg	aca	aat	gag	att	gtt	aca	ctc	aac	tat	ttg	gaa	cct	cgg	aca	gaa	1536
159	Val	Thr	Asn	Glu	Ile	Val	Thr	Leu	Asn	Tyr	Leu	Glu	Pro	Arg	Thr	Glu	
160				500						505				510			
162	tat	gaa	ctc	tgt	gtg	caa	ctg	gtc	cgt	cgt	gga	gag	ggt	ggg	gaa	ggg	1584
163	Tyr	Glu	Leu	Cys	Val	Gln	Leu	Val	Arg	Arg	Gly	Glu	Gly	Gly	Glu	Gly	
164		515						520					525				
166	cat	cct	gga	cct	gtg	aga	cgc	ttc	aca	aca	gct	tct	atc	gga	ctc	cct	1632
167	His	Pro	Gly	Pro	Val	Arg	Arg	Phe	Thr	Thr	Ala	Ser	Ile	Gly	Leu	Pro	
168		530					535						540				
170	cct	cca	aga	ggt	cta	aat	ctc	ctg	cct	aaa	agt	cag	acc	act	cta	aat	1680
171	Pro	Pro	Arg	Gly	Leu	Asn	Leu	Leu	Pro	Lys	Ser	Gln	Thr	Thr	Leu	Asn	
172	545				550						555				560		
174	ttg	acc	tgg	caa	cca	ata	ttt	cca	agc	tcg	gaa	gat	gac	ttt	tat	gtt	1728
175	Leu	Thr	Trp	Gln	Pro	Ile	Phe	Pro	Ser	Ser	Glu	Asp	Asp	Phe	Tyr	Val	
176				565						570				575			
178	gaa	gtg	gag	aga	agg	tct	gtg	caa	aaa	agt	gat	cag	cag	aat	att	aaa	1776
179	Glu	Val	Glu	Arg	Arg	Ser	Val	Gln	Lys	Ser	Asp	Gln	Gln	Asn	Ile	Lys	
180				580					585					590			
182	gtt	cca	ggc	aac	ttg	act	tcg	gtg	cta	ctt	aac	aac	tta	cat	ccc	agg	1824
183	Val	Pro	Gly	Asn	Leu	Thr	Ser	Val	Leu	Leu	Asn	Asn	Leu	His	Pro	Arg	
184			595					600					605				
186	gag	cag	tac	gtg	gtc	cga	gct	aga	gtc	aac	acc	aag	gcc	cag	ggg	gaa	1872
187	Glu	Gln	Tyr	Val	Val	Arg	Ala	Arg	Val	Asn	Thr	Lys	Ala	Gln	Gly	Glu	
188		610					615				620						
190	tgg	agt	gaa	gat	ctc	act	gct	tgg	acc	ctt	agt	gac	att	ctt	cct	cct	1920
191	Trp	Ser	Glu	Asp	Leu	Thr	Ala	Trp	Thr	Leu	Ser	Asp	Ile	Leu	Pro	Pro	

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192	625		630		635		640	
194	caa cca gaa aac atc aag att tcc aac att aca cac tcc tcg gct gtg	1968						
195	Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val							
196			645		650		655	
198	att tct tgg aca ata ttg gat ggc tat tct att tct tct att act atc	2016						
199	Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile							
200			660		665		670	
202	cgt tac aag gtt caa ggc aag aat gaa gac cag cac gtt gat gtg aag	2064						
203	Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys							
204			675		680		685	
206	ata aag aat gcc acc atc att cag tat cag ctc aag ggc cta gag cct	2112						
207	Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro							
208			690		695		700	
210	gaa aca gca tac cag gtg gac att ttt gca gag aac aac ata ggg tca	2160						
211	Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser							
212	705		710		715		720	
214	agc aac cca gcc ttt tct cat gaa ctg gtg acc ctc cca gaa tct caa	2208						
215	Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln							
216			725		730		735	
218	gca cca gcg gac ctc gga ggg ggg aag atg ctg ctt ata gcc atc ctt	2256						
219	Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu							
220			740		745		750	
222	ggc tct gct gga atg acc tgc ctg act gtg ctg ttg gcc ttt ctg atc	2304						
223	Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile							
224			755		760		765	
226	ata ttg caa ttg aag agg gca aat gtg caa agg aga atg gcc caa gcc	2352						
227	Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala							
228			770		775		780	
230	ttc caa aac gtg agg gaa gaa cca gct gtg cag ttc aac tca ggg act	2400						
231	Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr							
232	785		790		795		800	
234	ctg gcc cta aac agg aag gtc aaa aac aac cca gat cct aca att tat	2448						
235	Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr							
236			805		810		815	
238	cca gtg ctt gac tgg aat gac atc aaa ttt caa gat gtg att ggg gag	2496						
239	Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu							
240			820		825		830	
242	ggc aat ttt ggc caa gtt ctt aag gcg cgc atc aag aag gat ggg tta	2544						
243	Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu							
244			835		840		845	
246	cgg atg gat gct gcc atc aaa aga atg aaa gaa tat gcc tcc aaa gat	2592						
247	Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp							
248			850		855		860	
250	gat cac agg gac ttt gca gga gaa ctg gaa gtt ctt tgt aaa ctt gga	2640						
251	Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly							
252	865		870		875		880	
254	cac cat cca aac atc atc aat ctc tta gga gca tgt gaa cat cga ggc	2688						
255	His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly							
256			885		890		895	

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258 tac ttg tac ctg gcc att gag tac gcg ccc cat gga aac ctt ctg gac 2736
259 Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp
260          900          905          910
262 ttc ctt cgc aag agc cgt gtg ctg gag acg gac cca gca ttt gcc att 2784
263 Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile
264          915          920          925
266 gcc aat agc acc gcg tcc aca ctg tcc tcc cag cag ctc ctt cac ttc 2832
267 Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe
268          930          935          940
270 gct gcc gac gtg gcc cgg ggc atg gac tac ttg agc caa aaa cag ttt 2880
271 Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe
272 945          950          955          960
274 atc cac agg gat ctg gct gcc aga aac att tta gtt ggt gaa aac tat 2928
275 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr
276          965          970          975
278 gtg gca aaa ata gca gat ttt gga ttg tcc cga ggt caa gag gtg tac 2976
279 Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr
280          980          985          990
282 gtg aaa aag aca atg gga agg ctc cca gtg cgc tgg atg gcc atc gag 3024
283 Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu
284          995          1000          1005
286 tca ctg aat tac agt gtg tac aca acc aac agt gat gta tgg tcc tat 3072
287 Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr
288          1010          1015          1020
290 ggt gtg tta cta tgg gag att gtt agc tta gga ggc aca ccc tac tgc 3120
291 Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys
292 1025          1030          1035          1040
294 ggg atg act tgt gca gaa ctc tac gag aag ctg ccc cag ggc tac aga 3168
295 Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg
296          1045          1050          1055
298 ctg gag aag ccc ctg aac tgt gat gat gag gtg tat gat cta atg aga 3216
299 Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg
300          1060          1065          1070
302 caa tgc tgg cgg gag aag cct tat gag agg cca tca ttt gcc cag ata 3264
303 Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile
304          1075          1080          1085
306 ttg gtg tcc tta aac aga atg tta gag gag cga aag acc tac gtg aat 3312
307 Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn
308          1090          1095          1100
310 acc acg ctt tat gag aag ttt act tat gca gga att gac tgt tct gct 3360
311 Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala
312 1105          1110          1115          1120
314 gaa gaa gcg gcc 3372
315 Glu Glu Ala Ala
319 <210> SEQ ID NO: 2
320 <211> LENGTH: 1124
321 <212> TYPE: PRT
322 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 2

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**VERIFICATION SUMMARY**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date